

FIG. 1A

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTGGGG
 TTCAAGATCACTGGGACCAGGCCGTATCTATGCCGAGTCTAACCTCAACTGTC
 ACCCCAAGGCACTTGGACGTCCCTGGACAGACCGAGTCCCAGGAAGCCCCAGCACTGCC

 GCTGCCACACTGCCCTGAGCCCAAATGGGGAGTGAGAGGCCA TAG CTG TCT GGC
 S1 S5 S10 S15
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
 ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CCA CTG GTG CTC
 216 225 234 243 252
 S20 S25 S29 1
 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
 CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG
 261 270 279 288 297
 5 10 15
 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
 GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC
 306 315 324 333 342
 20 25 30
 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
 CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
 351 360 369 378 387
 35 40 45
 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG
 396 405 414 423 432
 50 55 60
 Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
 GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC
 441 450 459 468 477
 65 70 75
 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
 GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC
 486 495 504 513 522
 80 85 90
 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC
 531 540 549 558 567

FIG. 1B

95	100	105
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr		
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT		
576	585	594
603		612
110	115	120
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu		
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC		
621	630	639
648		657
125	130	135
Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val		
AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG		
666	675	684
693		702
140	145	150
Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val		
TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC		
711	720	729
738		747
155	160	165
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys		
TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC		
756	765	774
783		792
170	175	180
Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr		
CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC		
801	810	819
828		837
185	190	195
Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu		
ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA		
846	855	864
873		882
200	205	210
Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys		
TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG		
891	900	909
918		927
215	220	225
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys		
TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA		
936	945	954
963		972
230	235	240
Glu Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn		
GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC		
981	990	999
1008		1017

FIG. 1C

245	250	255
Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe		
CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC		
1026	1035	1044
1053	1062	
260	265	270
Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr		
AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC		
1071	1080	1089
1098	1107	
275	280	285
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala		
CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA		
1116	1125	1134
1143	1152	
290	295	300
Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala		
CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC		
1161	1170	1179
1188	1197	
305	310	315
Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala		
TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC		
1206	1215	1224
1233	1242	
320	325	330
His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr		
CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC		
1251	1260	1269
1278	1287	
335	340	
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp		
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AA <u>GGAATTC</u>		
1296	1305	1314
1323	1332	

FIG. 2

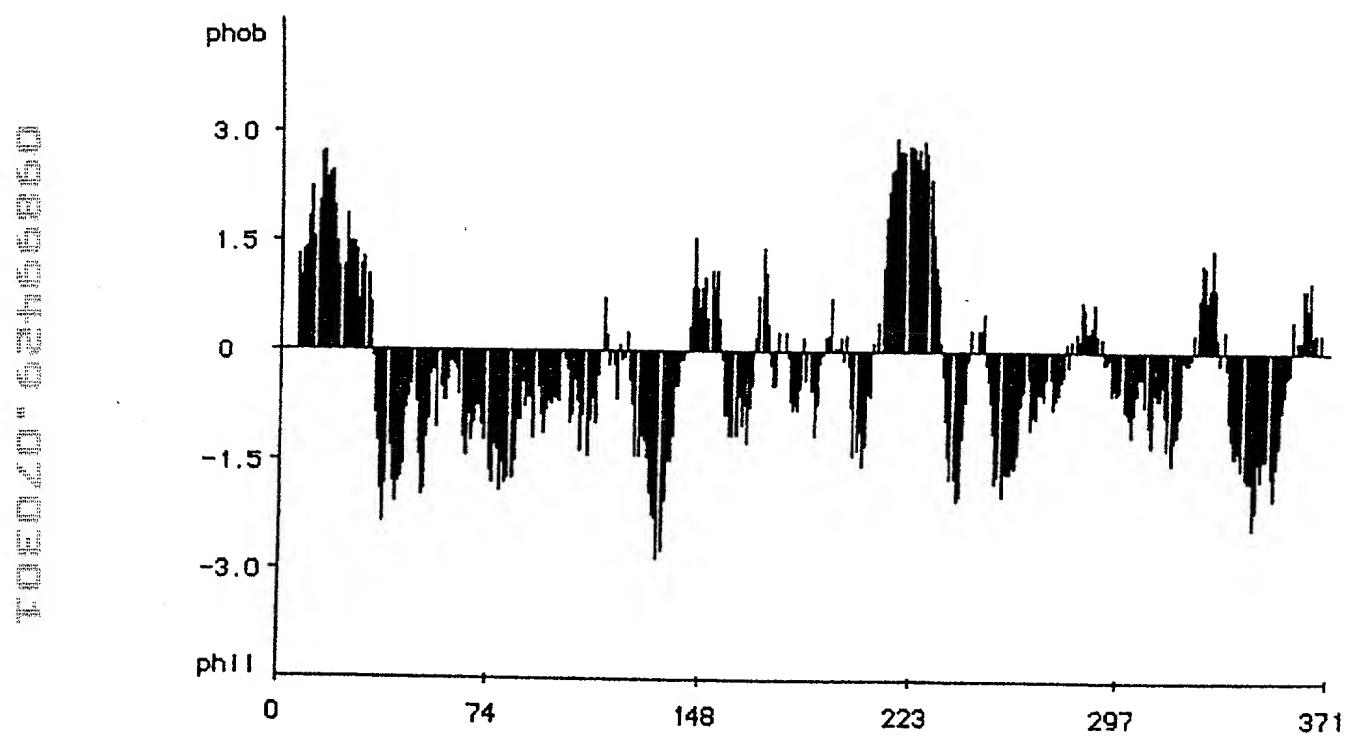


FIG. 3A

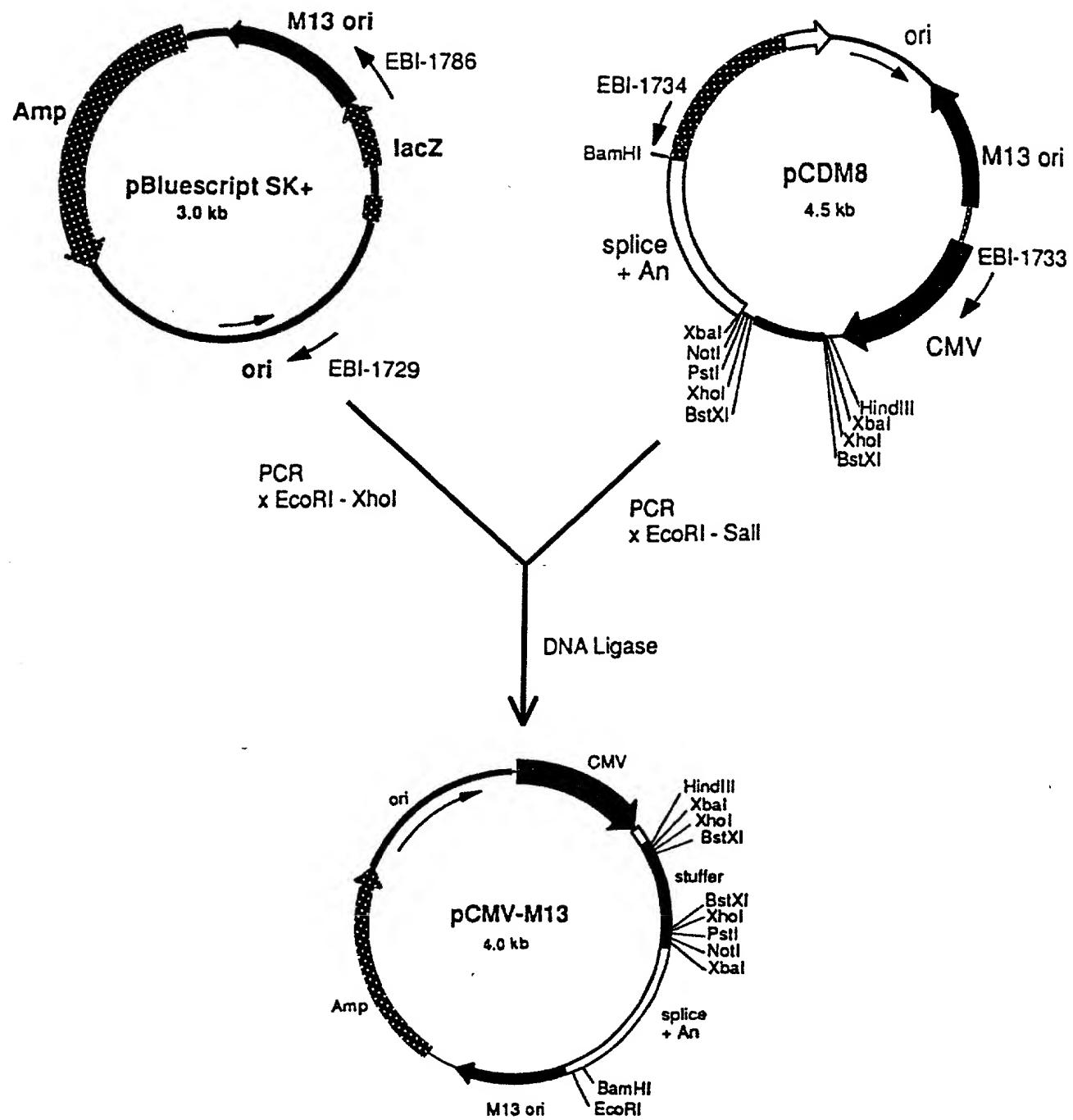


FIG. 3B

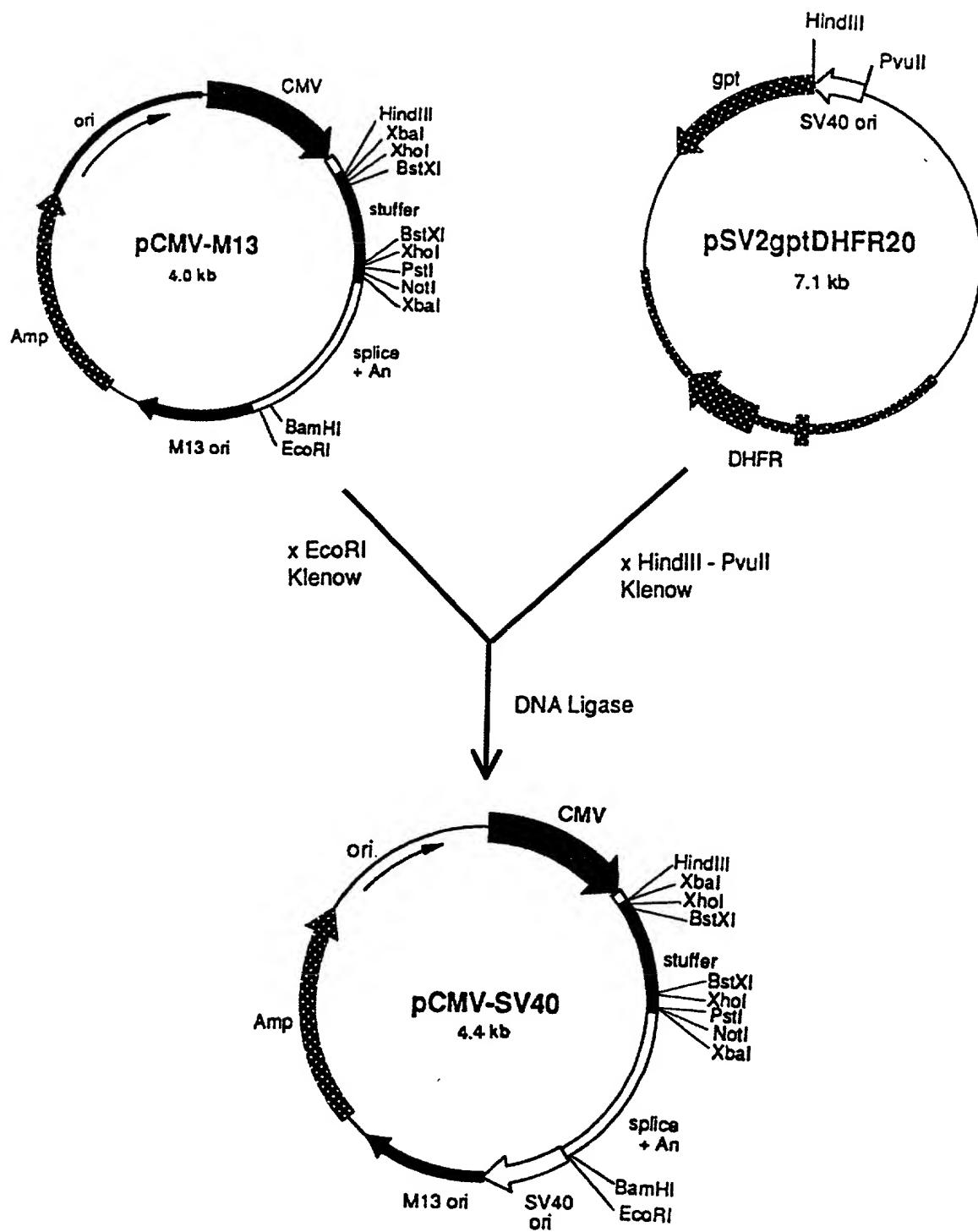


FIG. 4A

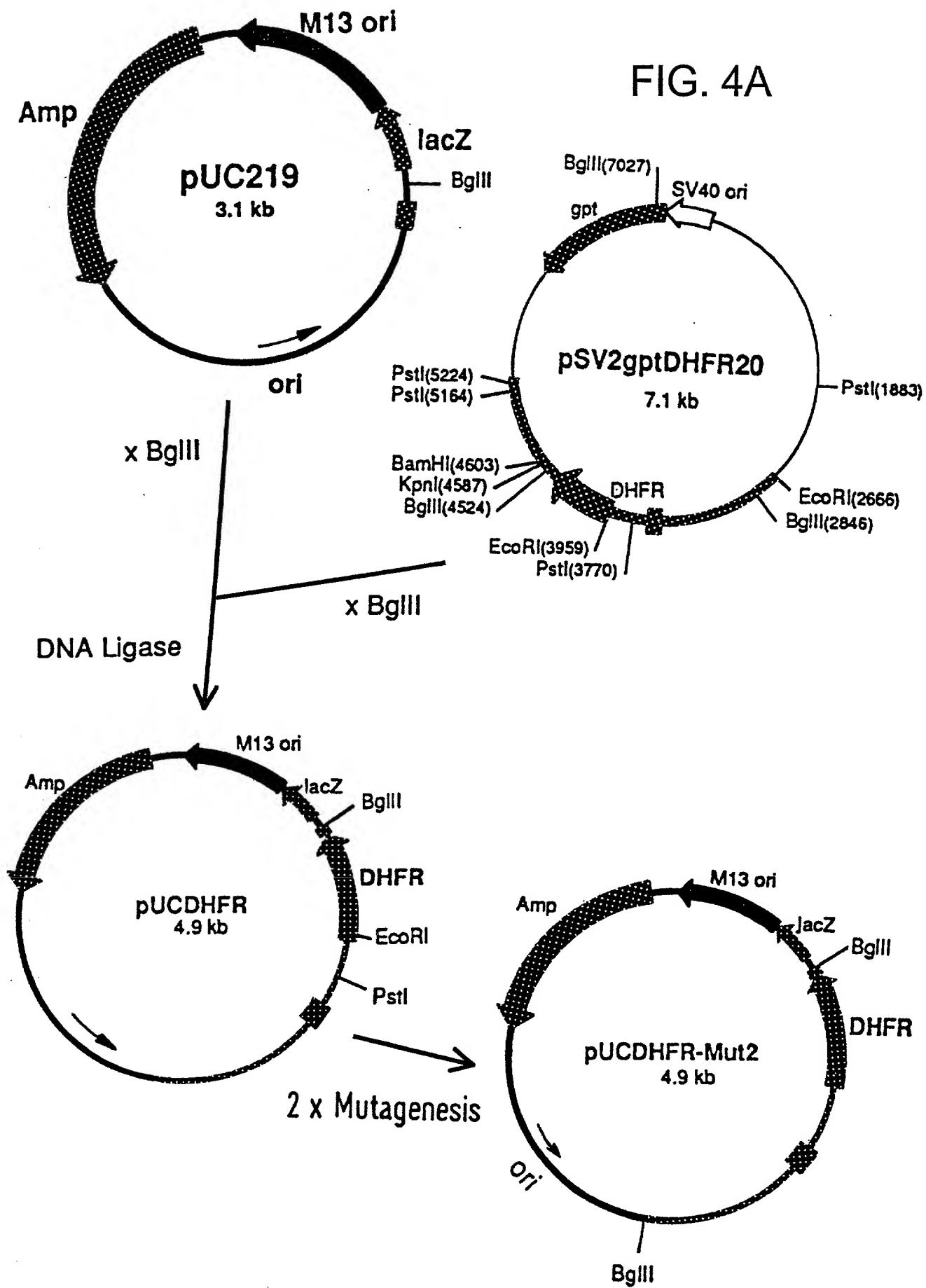


FIG. 4B

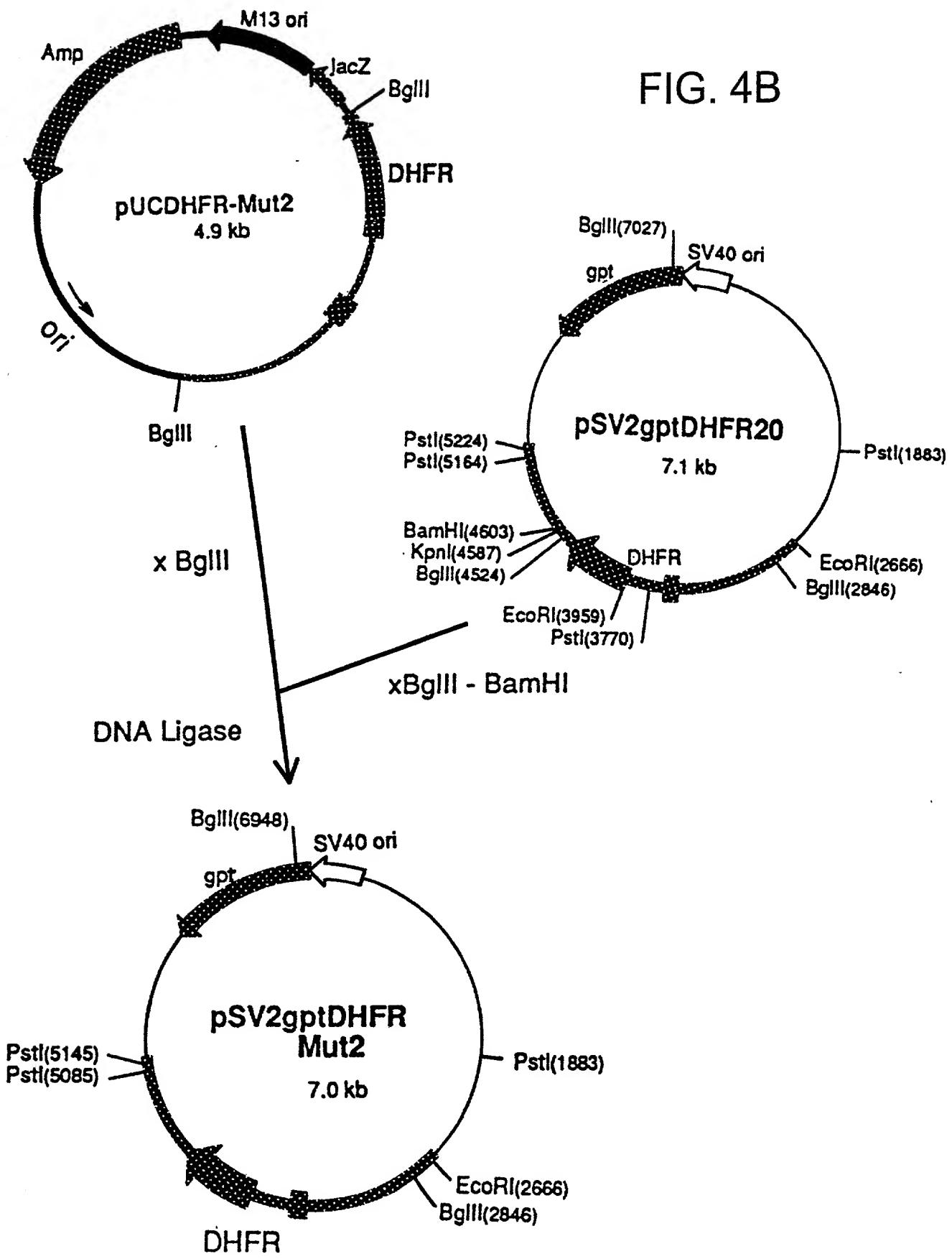


FIG. 5A

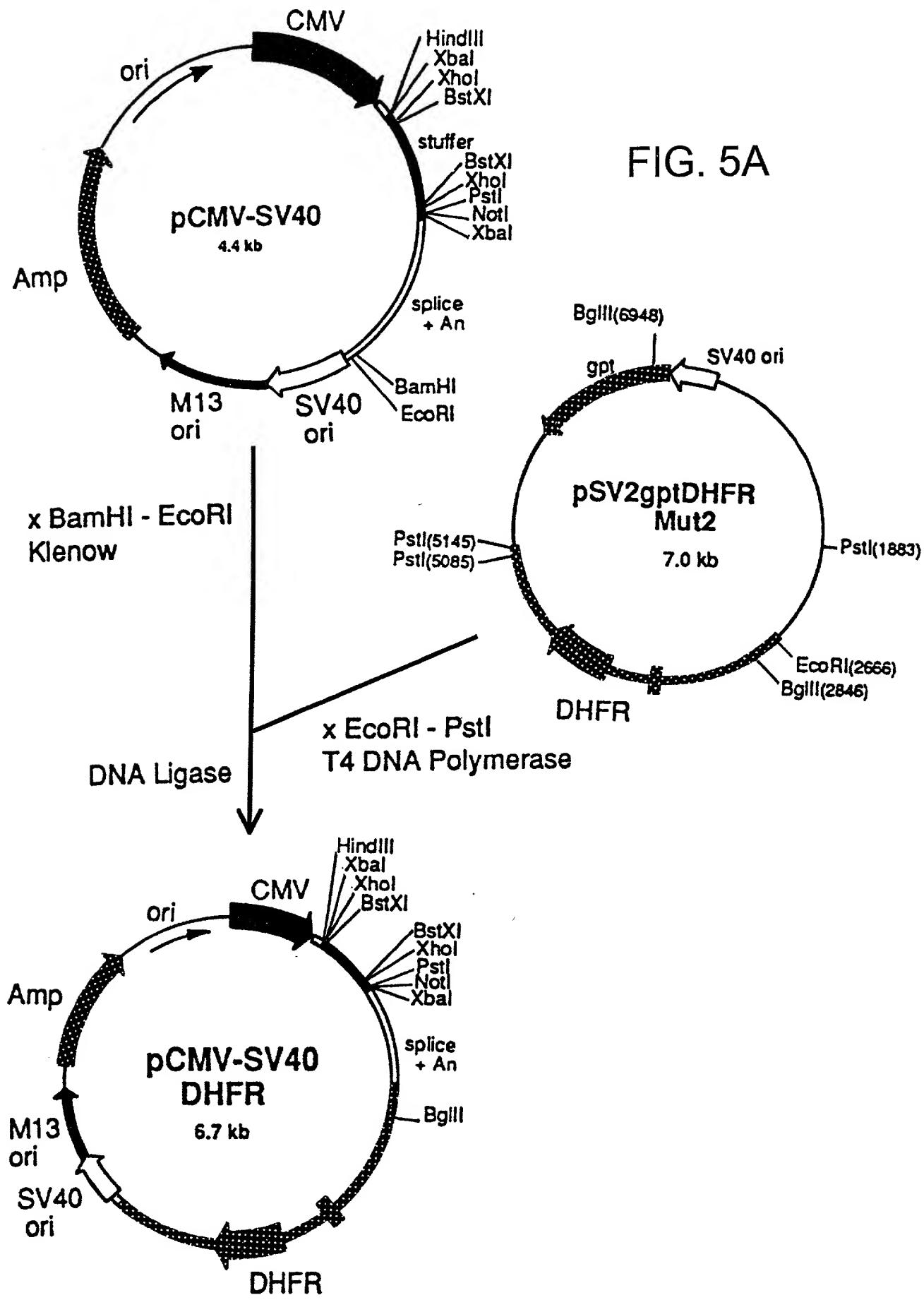


FIG. 5B

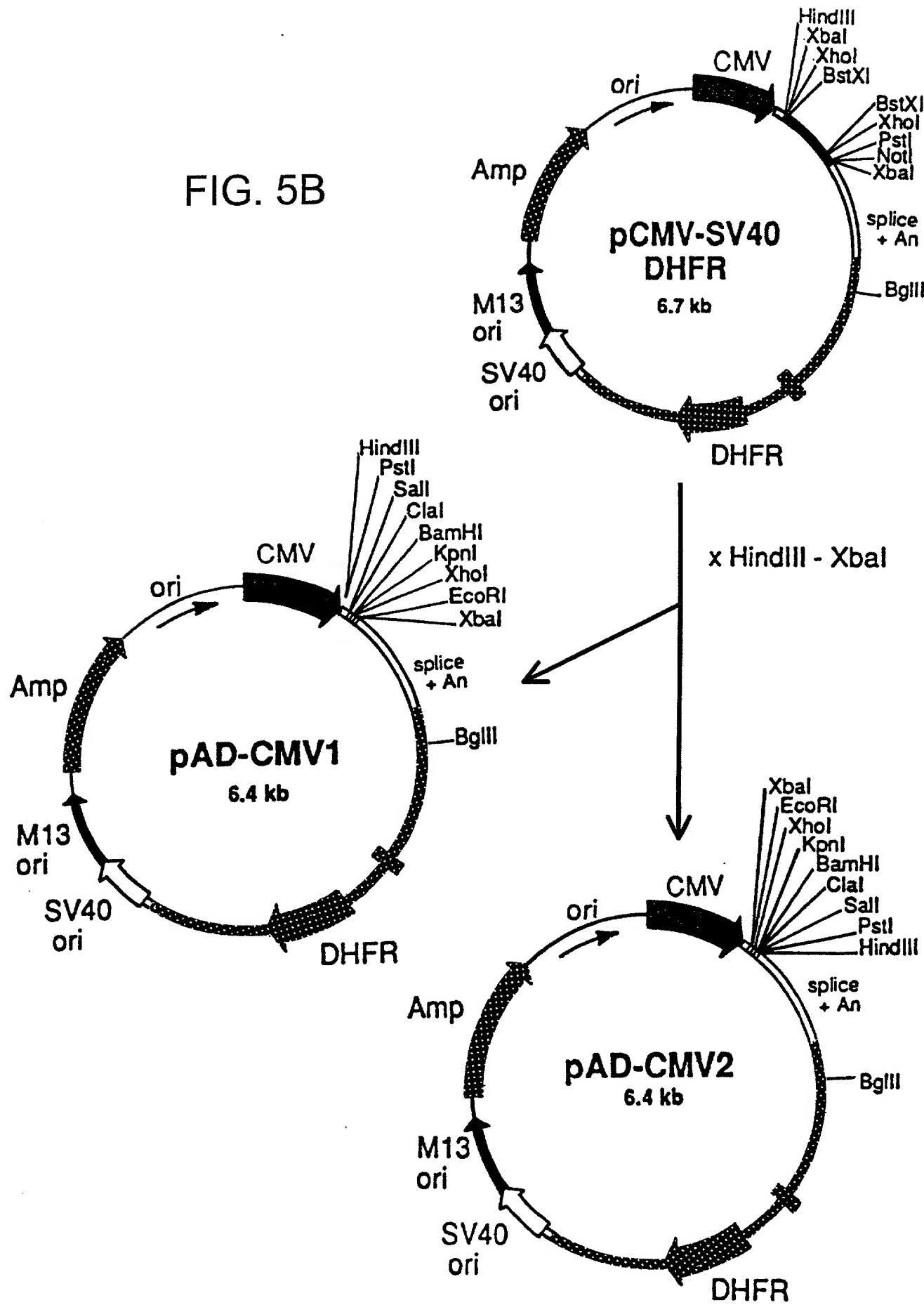


FIG. 6A

pAD-CMV1 : 6414 bp

TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT TAGTCATAG 60
CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG GCTGACCGCC 120
CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA CGCCAATAGG 180
GACTTTCCAT TGACGTCAAT GGGTGGAGTA TTTACGGTAA ACTGCCCACT TGGCAGTACA 240
TCAAGTGTAT CATATGCCAA GTACGCCCC TATTGACGTC AATGACGGTA AATGGCCCGC 300
CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTCCT ACTTGGCAGT ACATCTACGT 360
ATTAGTCATC GCTATTACCA TGGTGATGCG GTTTGCGAG TACATCAATG GGCGTGGATA 420
GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCATT GACGTCAATG GGAGTTGTT 480
TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC AACTCCGCC CATTGACGCA 540
AATGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC AGAGCTCTCT GGCTAACTAG 600
AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG 660
CTTCTGCAGG TCGACATCGA TGGATCCGGT ACCTCGAGCG CGAATTCTCT AGAGGATCTT 720
TGTGAAGGAA CCTTACTTCT GTGGTGTGAC ATAATTGGAC AAACTACCTA CAGAGATTAA 780
AAGCTCTAAG GTAAATATAA AATTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT 840
TGTGGTGTGTA TTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC 900
CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG ATGAGGCTAC 960
TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA 1020
CTTCCTTCA GAATTGCTAA GTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC 1080
TTGCTTTGCT ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA 1140
AAAATATTG ATGTATAGTG CCTTGACTAG AGATCATAAT CAGCCATACC ACATTTGTAG 1200
AGGTTTTACT TGCTTAAAAA AACCTCCCAC ACCTCCCCCT GAACCTGAAA CATAAAATGA 1260
ATGCAATTGT TGTTGTTAAC TTGTTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA 1320
GCATCACAAA TTTCACAAAT AAAGCATTTC TTTCACTGCA TTCTAGTTGT GGTTGTCCA 1380
AACTCATCAA TGTATCTTAT CATGTCTGGA TCAATTCTGA GAAACTAGCC TTAAAGACAG 1440

FIG. 6B

ACAGCTTGT TCTAGTCAGC CAGGCAAGCA TATGTAAATA AAGTTCTCA GGGAACTGAG	1500
GTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATT ACgtAAACAG AAGATTCCGC	1560
CTCAAGTTCC GGTTAACAAAC AGGAGGCAAC GAGATCTAA ATCTATTACT TCTAATCGGG	1620
TAATTAAAAC CTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG	1680
GCTCCGCCCT TCTCAGTACT CCCCACCCATT AGGCTCGCTA CTCCACCTCC ACTTCCGGC	1740
GCGACACCCA CGTGCCTCT CCCACCCGAC GCTAACCCCG CCCCTGCCCG TCTGACCCCG	1800
CCCACCAACCT GGCCCCGCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC GCAGCCAAGG	1860
CGGACGGGTA GACGCTGGGG GCGCTGAGGA GTGTCCTCT ACCTTCTCTG CTGGCTCGGT	1920
GGGGGACGCG GTGGATCTCA GGCTTCCGGA AGACTGGAAG AACCGGCTCA GAACCGCTTG	1980
TCTCCGCGGG GCTTGGCGG CGGAAGAATG GCCGCTAGAC GCGGACTTGG TGCGAGGCAT	2040
CGCAGGATGC AGAAGAGCAA GCCCGCCGGG AGCGCGCGGC TGTACTACCC CGCGCCTGGA	2100
GCGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC CTCGTGGAGG	2160
CGGGGCCTCT GATGTTCAAA TAGGATGCTA GGCTGTTGA GGCGTGGCCT CCGATTACAA	2220
AGTGGGAAGC AGCGCCGGGC GACTGCAATT TCGCGCCAAA CTTGGGGAA GCACAGCGTA	2280
CAGGCTGCCT AGGTGATCGC TGCTGCTGTC ATGGTTCGAC CGCTGAAC TG CATCGTCGCC	2340
GTGTCCCAGA ATATGGGCAT CGGCAAGAAC GGAGACCTTC CCTGGCCAAT GCTCAGGTAC	2400
TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG CACTTGGCGG	2460
AGACGCGCGG GCCAACTACT TAGGGACAGT CATGAGGGGT AGGCCCCGCCG GCTGCTGCC	2520
TTGCCCATGC CCGCGGTGAT CCCCATGCTG TGCCAGCCTT TGCCAGAGG CGCTCTAGCT	2580
GGGAGCAAAG TCCGGTCACT GGGCAGCACC ACCCCCCGGA CTTGCATGGG TAGCCGCTGA	2640
GATGGAGCCT GAGCACACGT GACAGGGTCC CTGTTAACGC AGTGTTCCTC TAACTTCAG	2700
GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAAG GTAAACAGAA	2760
CCTGGTGATT ATGGGCCGGA AAACCTGGTT CTCCATTCCCT GAGAAGAAC GACCTTAAA	2820
GGACAGAATT AATATAGTTC TCAGTAGAGA GCTCAAGGAA CCACCACAAG GAGCTCATT	2880
TCTTGCCAAA AGTCTGGACC ATGCCTAAA ACTTATTGAA CAACCAGAGT TAGCAGATAA	2940
AGTGGACATG GTTGGATAG TTGGAGGCAG TTCCGTTAC AAGGAAGCCA TGAATCAGCC	3000

FIG. 6C

AGGCCATCTC AGACTCTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG ACACGTTCTT	3060
CCCAGAAATT GATTGGAGA AATATAAACT TCTCCCAGAG TACCCAGGGG TCCTTCTGA	3120
AGTCCAGGAG GAAAAGGCA TCAAGTATAA ATTTGAAGTC TATGAGAAGA AAGGCTAAC	3180
GAAAGATACT TGCTGATTGA CTTCAAGTTC TACTGTTTC CTCCTAAAT TATGCATTT	3240
TACAAGACCA TGGGACTTGT GTTGGCTTTA GATCCTGTGC ATCCTGGGCA ACTGTTGTAC	3300
TCTAAGCCAC TCCCCAAAGT CATGCCCGAG CCCCTGTATA ATTCTAAACA ATTAGAATT	3360
TTTCATTT CATTAGTCTA ACCAGGTTAT ATTAAATATA CTTAAGAAA CACCATTG	3420
CATAAAAGTTC TCAATGCCCG TCCCATGCAG CCTCAAGTGG CTCCCCAGCA GATGCATAGG	3480
GTAGTGTGTG TACAAGAGAC CCCAAAGACA TAGAGCCCT GAGAGCATGA GCTGATATGG	3540
GGGCTCATAG AGATAGGAGC TAGATGAATA AGTACAAAGG GCAGAAATGG GTTTAACCA	3600
GCAGAGCTAG AACTCAGACT TTAAAGAAAA TTAGATCAA GTAGAGACTG AATTATTCTG	3660
CACATCAGAC TCTGAGCAGA GTTCTGTTCA CTCAGACAGA AAATGGGTAA ATTGAGAGCT	3720
GGCTCCATTG TGCTCCTTAG AGATGGGAGC AGGTGGAGGA TTATATAAGG TCTGGAACAT	3780
TTAACTTCTC CGTTCTCAT CTTCAGTGAG ATTCCAAGGG ATACTACAAT TCTGTGGAAT	3840
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC	3900
ATGCATCTCA ATTAGTCAGC AACCAAGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA	3960
AGTATGCAA GCATGCATCT CAATTAGTCA GCAACCATAG TCCCGCCCCCT AACTCCGCC	4020
ATCCCGCCCC TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT	4080
TTTATTTATG CAGAGGCCGA GGCGCCTCTG AGCTATTCCA GAAGTAGTGA GGAGGCTTT	4140
TTGGAGGCCT AGGCTTTGC AAAAAAGCTA ATTCAAGCCTG AATGGCGAAT GGGACGCGCC	4200
CTGTAGCGGC GCATTAAGCG CGCGGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT	4260
TGCCAGCGCC CTAGCGCCCCG CTCCTTCGC TTTCTCCCT TCCTTCTCG CCACGTTCGC	4320
CGGCTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTA GGGTTCCGAT TTAGTGCTTT	4380
ACGGCACCTC GACCCAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC	4440
TGATAGACGG TTTTCGCC CTTGACGTTG GAGTCCACGT TCTTAATAG TGGACTCTTG	4500
TTCCAAACTG GAACAACACT CAACCCATAC TCGGTCTATT CTTTGATTT ATAAGGGATT	4560

FIG. 6D

TTGCCGATT	CGGCCTATTG	GTTAAAAAAT	GAGCTGATT	AACAAAATT	TAACGCGAAT	4620
TTAACAAA	TATTAACGTT	TACAATTCA	GGTGGCACTT	TTCGGGAAA	TGTGCGCGGA	4680
ACCCCTATTT	GTTATTTT	CTAAATACAT	TCAAATATGT	ATCCGCTCAT	GAGACAATAA	4740
CCCTGATAAA	TGCTTCAATA	ATATTGAAAA	AGGAAGAGTA	TGAGTATTCA	ACATTCCGT	4800
GTCGCCCTA	TTCCCTTTT	TGCGGCATT	TGCCTCCTG	TTTTGCTCA	CCCAGAAACG	4860
CTGGTGAAAG	TAAAAGATGC	TGAAGATCAG	TTGGGTGCAC	GAGTGGGTTA	CATCGAACTG	4920
GATCTCAACA	GCGGTAAGAT	CCTTGAGAGT	TTTCGCCCCG	AAGAACGTTT	TCCAATGATG	4980
AGCACTTTA	AAGTTCTGCT	ATGTGGCGCG	GTATTATCCC	GTATTGACGC	CGGGCAAGAG	5040
CAACTCGGTC	GCCGCATACA	CTATTCTCAG	AATGACTTGG	TTGAGTACTC	ACCAGTCACA	5100
GAAAAGCATC	TTACGGATGG	CATGACAGTA	AGAGAATTAT	GCAGTGCTGC	CATAACCATG	5160
AGTGATAACA	CTGCGGCCAA	CTTACTTCTG	ACAACGATCG	GAGGACCGAA	GGAGCTAAC	5220
GCTTTTTGC	ACAACATGGG	GGATCATGTA	ACTCGCCTTG	ATCGTTGGGA	ACCGGAGCTG	5280
AATGAAGCCA	TACCAAACGA	CGAGCGTGAC	ACCACGATGC	CTGTAGCAAT	GGCAACAAACG	5340
TTGCGCAAAC	TATTAACCTGG	CGAACTACTT	ACTCTAGCTT	CCCGGCAACA	ATTAATAGAC	5400
TGGATGGAGG	CGGATAAAAGT	TGCAGGACCA	CTTCTGCGCT	CGGCCCTTCC	GGCTGGCTGG	5460
TTTATTGCTG	ATAAATCTGG	AGCCGGTGAG	CGTGGGTCTC	GCGGTATCAT	TGCAGCACTG	5520
GGGCCAGATG	GTAAGCCCTC	CCGTATCGTA	GTTATCTACA	CGACGGGGAG	TCAGGCAACT	5580
ATGGATGAAC	GAAATAGACA	GATCGCTGAG	ATAGGTGCCT	CACTGATTAA	GCATTGGTAA	5640
CTGTCAGACC	AAGTTTACTC	ATATATACTT	TAGATTGATT	AAAAACTTCA	TTTTAATT	5700
AAAAGGATCT	AGGTGAAGAT	CCTTTTGAT	AATCTCATGA	CCAAAATCCC	TTAACGTGAG	5760
TTTCGTTCC	ACTGAGCGTC	AGACCCGTA	GAAAAGATCA	AAGGATCTTC	TTGAGATCCT	5820
TTTTTCTGC	GCGTAATCTG	CTGCTTGCAA	ACAAAAAAAC	CACCGCTACC	AGCGGTGGTT	5880
TGTTTGCAGG	ATCAAGAGCT	ACCAACTCTT	TTTCCGAAGG	TAACTGGCTT	CAGCAGAGCG	5940
CAGATACCAA	ATACTGTCT	TCTAGTGTAG	CCGTAGTTAG	GCCACCACCT	CAAGAACTCT	6000
GTAGCACCAGC	CTACATACCT	CGCTCTGCTA	ATCCTGTTAC	CAGTGGCTGC	TGCCAGTGGC	6060
GATAAGTCGT	GTCTTACCGG	GTTGGACTCA	AGACGATAGT	TACCGGATAA	GGCGCAGCGG	6120

FIG. 6E

TCGGGCTGAA CGGGGGGTTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA 6180
CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG 6240
GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGG GCTTCCAGGG 6300
GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA 6360
TTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCC

FIG. 7A

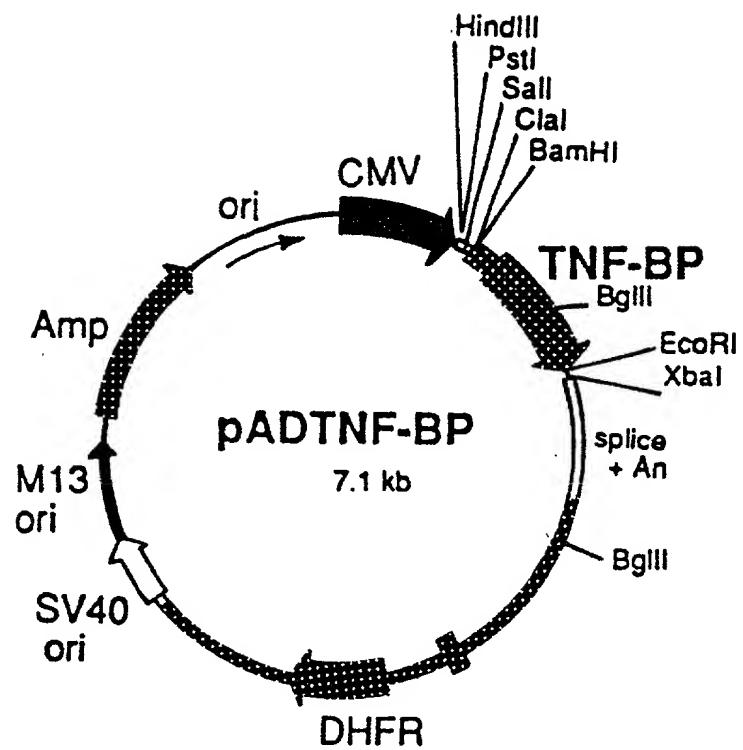


FIG. 7B

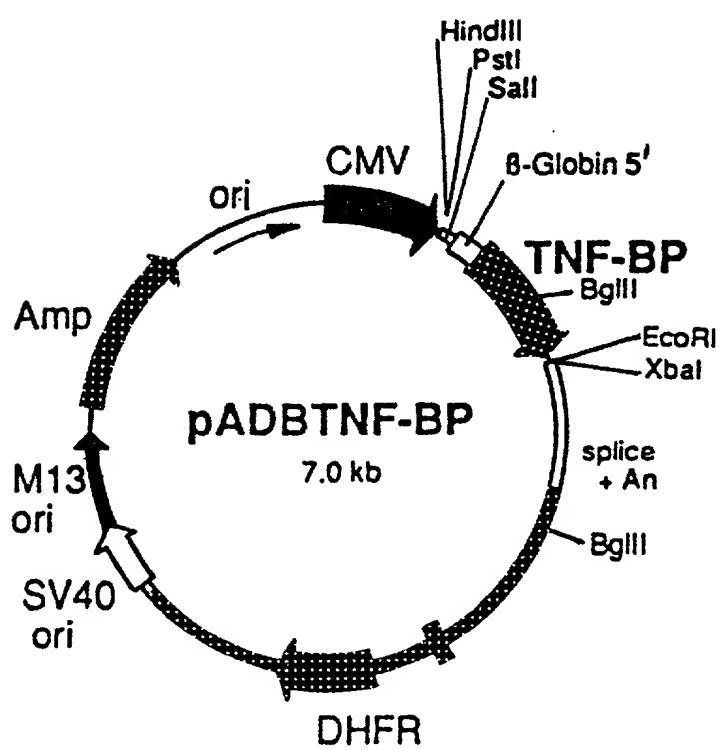


FIG. 7C

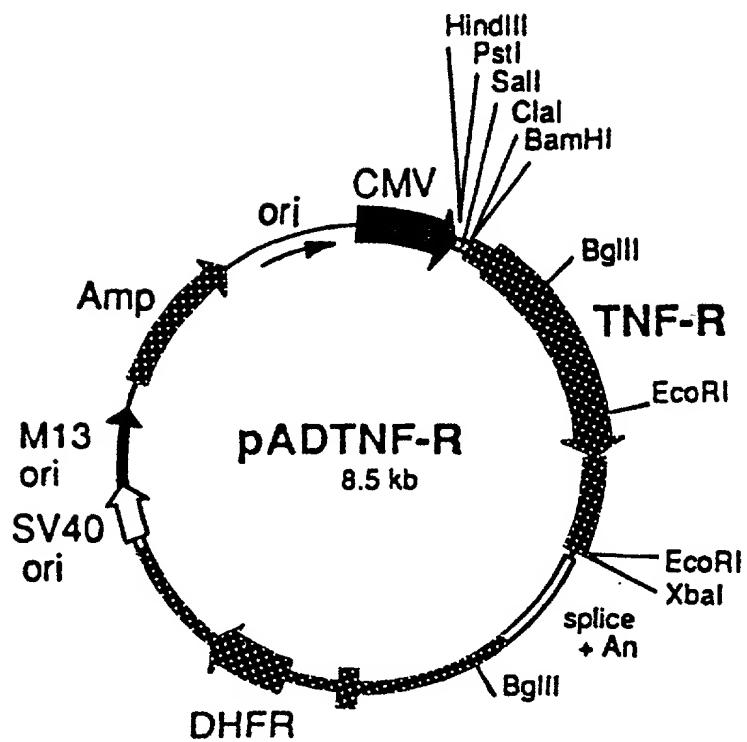


FIG. 7D

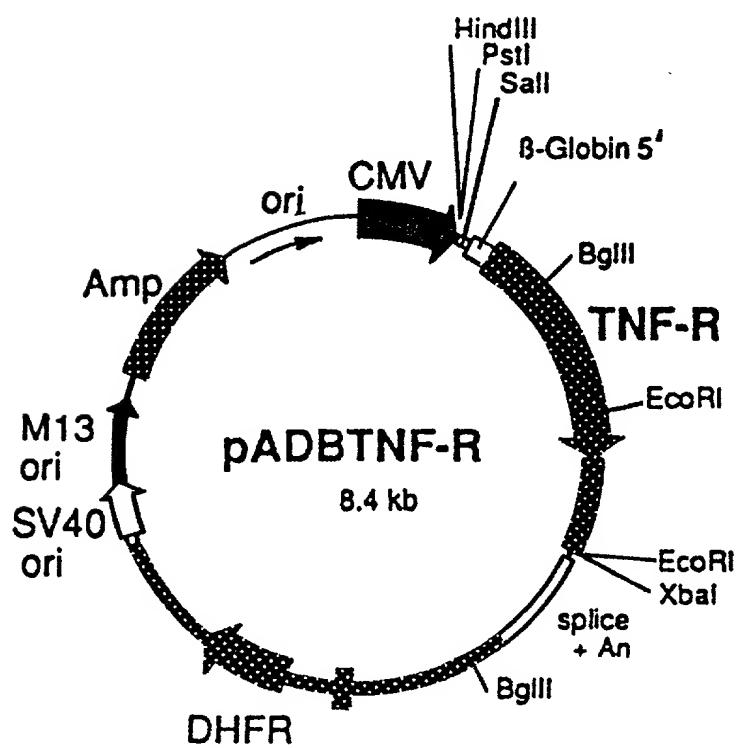


FIG. 8A

ratTNF-R

GAATTCCCTTT TCTCCGAGTT TTCTGAACCTC TGGCTCATGA TCGGGCTTAC TGGATACGAG 60
 AATCCTGGAG, GACCGTACCC TGATTTCCAT CTACCTCTGA CTTTGAGCCT TTCTAACCCG 120
 GGGCTCACGC TGCCAACACC CGGGCCACCT GGTCCGATCG TCTTACTTCA TTCACCAGCG 180
 TTGCCAATTG CTGCCCTGTC CCCAGCCCCA ATGGGGGAGT GAGAGAGGCC ACTGCCGGCC 240
 GGAC
 245/1 275/11
 ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG
 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Ala Leu Leu Met
 305/21 335/31
 GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG
 Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg
 365/41 395/51
 GAT AAT TTG TGT CCC CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC
 Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr
 425/61 455/71
 AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC
 Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val
 485/81 515/91
 TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC
 Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu
 545/101 575/111
 AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC
 Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp
 605/121 635/131
 ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT
 Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His
 665/141 695/151
 TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG
 Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu
 725/161 755/171
 AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC
 Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr
 785/181 815/191
 CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA
 Pro Cys Ser His Cys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala
 845/201 875/211
 AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA
 Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu
 905/221 935/231
 GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG
 Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg
 965/241 995/251
 CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA
 Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu
 1025/261 1055/271
 GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC
 Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly
 1085/281 1115/291
 TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC
 Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr
 1145/301 1175/311
 CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG
 Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu
 1205/321 1235/331
 GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC
 Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile

FIG. 8B

1265/341	1295/351
CCC GCC CCT GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT	
Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr	
1325/361	1355/371
GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG	
Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu	
1385/381	1415/391
TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG	
Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly	
1445/401	1475/411
CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA	
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg	
1505/421	1535/431
CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC	
His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys	
1565/441	1595/451
CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG	
Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro	
1625/461	
CGA TAA	
Arg Stop	
GGCCACACCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT	1680
GCCCTGCTTC CCTGTGAACC TCCTCTTGG TCCTCTAGGG GGCAGGGCTCG ATCTGGCAGG	1740
CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGTT GTACATAGCT TTTCCCAGCT	1800
GCCGAGGACA GCCTGTGCCA GCCACTTGTG CATGGCAGGG AAGTGTGCCA TCTGCTCCCCA	1860
GACAGCTGAG GGTGCCAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT	1920
GATACCCACT TGGGATGCAA GGACCCAAAC AAAGCTTCTC AGGGCCTCCT CAGTTGATT	1980
CTGGGCCCTT TTCACAGTAG ATAAAAACAGT CTTGTATTG ATTATATCAC ACTAATGGAT	2040
GAACGGTTGA ACTCCCTAAG GTAGGGCAA GCACAGAACAA GTGGGGTCTC CAGCTGGAGC	2100
CCCCGACTCT TGTAAATACA CTAAAAATCT AAAAGTGAAG AAAAAGGAA AAAAAGGAA	2160
TTC	

FIG. 9A

huTNF-R

GAATTCTCTG, GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC TGGGACCAGG 60
 CGGTGATCTC TATGCCGAG TCTCAACCCT CAACTGTCAC CCCAAGGCAC TTGGGACGTC 120
 CTGGACAGAC CGAGTCCCAG GAAGCCCCAG CACTGCGCT GCCACACTGC CCTGAGCCCA 180
 AATGGGGAG TGAGAGGCCA TAGCTGTCTG GC

213/1 243/11
 ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC CTG GAG CTG TTG GTG
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val
 273/21 303/31
 GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA
 Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg
 333/41 363/51
 GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
 393/61 423/71
 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC
 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 453/81 483/91
 TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC
 Cys Arg Glu Cys Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu
 513/101 543/111
 AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC
 Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 573/121 603/131
 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu
 633/141 663/151
 TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG
 Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 693/161 723/171
 AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
 753/181 783/191
 TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG
 Ser Cys Ser Asn Cys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
 813/201 843/211
 AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT
 Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe
 873/221 903/231
 GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG
 Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
 933/241 963/251
 TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu
 993/261 1023/271
 GGA ACT ACT AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC
 Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr
 1053/281 1083/291
 CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC
 Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
 1113/301 1143/311
 CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG
 Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 1173/321 1203/331
 GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys

HuTNF-R cDNA

FIG. 9B

1233/341	1263/351
TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC	
Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr	
1293/361	1323/371
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG	
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu	
1353/381	1383/391
AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA	
Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln	
1413/401	1443/411
TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG	
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu	
1473/421	1503/431
CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG	
Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala	
1533/441	1563/451
CTT TGC GGC CCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGA	1580
Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg Stop	

GGCTGCGCCC CTGCGGGCAG CTCTAAGGAC CGTCCTGCGA	1620
GATCGCCCTTC CAACCCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG	1680
CTAGCAGCCG CCTACTGGT GCTAACCCCT CGATGTACAT AGCTTTCTC AGCTGCCTGC	1740
GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT	1800
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTG GGTGTCCCTCA	1860
CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC CTTTTCAACA GTGCATAAGC	1920
AGTTTTTTT GTTTTGTT TGTTTTAAA TCAATCATGT TACACTAATA	1980
GAAACTTGGC ACTCCTGTGC CCTCTGCCTG GACAAGCACA TAGCAAGCTG AACTGTCCCTA	2040
AGGCAGGGC GAGCACGGAA CAATGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA	2100
CACTAAATT CTGAAGTTAA AAAAAAAA AAAAGGAATT C	2141

FIG.10

